

(FILE 'HOME' ENTERED AT 16:10:14 ON 17 APR 2002)

FILE 'BIOSIS, CAPLUS, SCISEARCH, LIFESCI, EMBASE' ENTERED AT 16:10:57 ON
17 APR 2002

L1	292 S BIOTIN SYNTHASE
L2	0 S L1 (A) MAIZE
L3	0 S L1 (A) ZEA MAYS
L4	124 DUPLICATE REMOVE L1 REMOVAL (168 DUPLICATES REMOVED)
L5	32 S L1 AND PLANT
L6	4 S L5 (A) CORN
L7	0 S L1 (A) CORN
L8	4 DUPLICATE REMOVE L6 REMOVAL (0 DUPLICATES REMOVED)

FILE 'USPATFULL, EUROPATFULL, JAPIO, PATOSWO' ENTERED AT 16:22:23 ON 17
APR 2002

L9	6 S L5
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L6 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2002 ACS
 AN 2001:817227 CAPLUS
 DN 135:368546
 TI Cloning, sequences and recombinant expression of **plant** biotin
 synthases
 IN Allen, Stephen M.; Kinney, Anthony J.; Miao, Guo-hua; Orozco, Emil M.
 PA USA
 SO U.S. Pat. Appl. Publ., 46 pp.
 CODEN: USXXCO
 DT Patent
 LA English
 IC ICM C12N009-00
 ICS C07H021-04; C12N015-82; C12N005-04
 NCL 435183000
 CC 7-5 (Enzymes)
 Section cross-reference(s): 3, 5, 11

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2001039042	A1	20011108	US 2000-740288	20001219
PRAI	US 1999-172929P	P	19991221		

AB This invention relates to an isolated nucleic acid fragment encoding a
 biotin synthases. Amino acid and encoding cDNA sequences of biotin
 synthases from barley, maize, prickly poppy, soybean and wheat are
 disclosed. The invention also relates to the construction of a chimeric
 gene encoding all or a portion of the biotin synthases, in sense or
 antisense orientation, wherein expression of the chimeric gene results in
 prodn. of altered levels of the biotin synthases in a transformed host
 cell.

ST **plant biotin synthase** cDNA sequence chimeric
 gene

IT Dicotyledon (Magnoliopsida)
 Monocotyledon (Liliopsida)

(biotin synthase chimeric gene expression in;
 cloning, sequences and recombinant expression of **plant** biotin
 synthases)

IT Gene, **plant**

RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BPR
 (Biological process); BSU (Biological study, unclassified); BUU
 (Biological use, unclassified); PRP (Properties); BIOL (Biological
 study);

PREP (Preparation); PROC (Process); USES (Uses)
 (chimeric; cloning, sequences and recombinant expression of
plant biotin synthases)

IT Bacteria (Eubacteria)

Plant cell

Yeast

(cloning host; cloning, sequences and recombinant expression of
plant biotin synthases)

IT Argemone mexicana

Barley

Corn

Molecular cloning

Protein sequences

Soybean (Glycine max)

Transformation, genetic

Wheat

cDNA sequences

(cloning, sequences and recombinant expression of **plant**

biotin synthases)

IT Chimeric gene
 RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
 PREP (Preparation); PROC (Process); USES (Uses)
 (**plant**; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT Transgene
 RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
 PREP (Preparation); USES (Uses)
 (**plant**; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT Herbicides
 (screening of; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT **Plant** (Embryophyta)
 (transgenic; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT 372993-05-0DP, subfragments are claimed 372993-06-1DP, subfragments are claimed 372993-07-2DP, subfragments are claimed 372993-08-3DP, subfragments are claimed 372993-09-4DP, subfragments are claimed 372993-10-7DP, subfragments are claimed 372993-11-8DP, subfragments are claimed 372993-12-9DP, subfragments are claimed 372993-13-0DP, subfragments are claimed 372993-14-1DP, subfragments are claimed 372993-15-2DP, subfragments are claimed 372993-16-3DP, subfragments are claimed 372993-17-4DP, subfragments are claimed 372993-18-5DP, subfragments are claimed 372993-19-6DP, subfragments are claimed 373384-78-2DP, subfragments are claimed
 RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
 PREP (Preparation); USES (Uses)
 (amino acid sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT 80146-93-6P, **Biotin synthase**
 RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
 PREP (Preparation); USES (Uses)
 (cloning, sequences and recombinant expression of **plant** biotin synthases)

IT 372992-89-7DP, subfragments are claimed
 RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (nucleotide sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT 372992-90-0D, subfragments are claimed 372992-91-1D, subfragments are claimed 372992-92-2D, subfragments are claimed 372992-93-3D, subfragments are claimed 372992-94-4D, subfragments are claimed 372992-95-5D, subfragments are claimed 372992-96-6D, subfragments are claimed 372992-97-7D, subfragments are claimed 372992-98-8D, subfragments are claimed 372992-99-9D, subfragments are claimed 372993-00-5D, subfragments are claimed 372993-01-6D, subfragments are claimed 372993-02-7D, subfragments are claimed 372993-03-8D, subfragments are claimed 372993-04-9D, subfragments are claimed

RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
 (nucleotide sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT 253862-81-6 372994-37-1 373384-02-2
 RL: PRP (Properties)
 (unclaimed protein sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)

IT 372994-38-2 372994-39-3
 RL: PRP (Properties)
 (unclaimed sequence; cloning, sequences and recombinant expression of **plant** biotin synthases)

L6 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2002 ACS
 AN 1999:104560 CAPLUS
 DN 130:163980
 TI Transgenic plants having increased biotin content
 IN Patton, David A.
 PA Novartis Finance Corporation, USA
 SO U.S., 34 pp., Cont.-in-part of U.S. Ser. No. 401,068.
 CODEN: USXXAM
 DT Patent
 LA English
 IC ICM A01H005-00
 ICS C12N005-04
 NCL 800278000
 CC 3-2 (Biochemical Genetics)
 Section cross-reference(s): 11, 18

FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5869719	A	19990209	US 1997-846338	19970430
	US 5859335	A	19990112	US 1995-401068	19950308
PRAI	US 1995-401068		19950308		
	US 1994-351970		19941208		

AB The invention reveals that biotin biosynthesis in a **plant** is enhanced when the level of one or more of the enzymes in the **plant** biotin biosynthetic pathway is increased. The nutritional value of plants as dietary sources of biotin is enhanced with this invention. Provided are methods of enhancing biotin levels by introducing into **plant** tissue a chimeric gene capable of expressing a biotin biosynthetic enzyme such as **biotin synthase** or DAP aminotransferase.

ST biotin biosynthesis nutrition chimeric **plant**; synthase biotin chimeric **plant**; diaminopelargonate aminotransferase chimeric **plant**

IT Bacteria (Eubacteria)
 (biotin biosynthetic enzyme from; transgenic plants having increased biotin content)

IT Escherichia coli
 (biotin biosynthetic enzymes from; transgenic plants having increased biotin content)

IT Enzymes, biological studies
 RL: AGR (Agricultural use); BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (biotin biosynthetic; transgenic plants having increased biotin content)

IT Genes (**plant**)

RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (chimeric, encoding biotin biosynthetic enzymes; transgenic plants having increased biotin content)

IT Nutrition (animal)
 (enhancement of in humans; transgenic plants having increased biotin content)

IT Arabidopsis thaliana
 Canola
 Corn
 Soybean (Glycine max)
 Tobacco
 Wheat
 (transgenic plants having increased biotin content)

IT Plant (Embryophyta)
 Plant cells
 Plant tissue
 (transgenic; transgenic plants having increased biotin content)

IT Chloroplast
 (transit peptide signal sequence from; transgenic plants having increased biotin content)

IT 37259-71-5P 80146-93-6P, Biotin synthase
 RL: AGR (Agricultural use); BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (biotin biosynthetic; transgenic plants having increased biotin content)

IT 9075-61-0P, 7-Keto-8-aminopelargonic acid synthetase 37259-75-9P, Desthiobiotin synthetase 55467-50-0P, Synthetase, pimelyl coenzyme a
 RL: AGR (Agricultural use); BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (transgenic plants having increased biotin content)

IT 58-85-5P, Biotin
 RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (transgenic plants having increased biotin content)

RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
- (2) Anon; GB 2216530 1989 CAPLUS
- (3) Anon; EP 0635572 1994 CAPLUS
- (4) Anon; WO 94/08023 1994 CAPLUS
- (5) Baldet; Genbank Access No L34413 Locus ATHSEACA 1995
- (6) Baldet, P; Eur J BioChem 1993, V217, P479 CAPLUS
- (7) Campbell; US 5445952 1995 CAPLUS
- (8) Dickson; Science 1975, V187, P27 CAPLUS
- (9) Eisenberg, M; Adv Enzymol 1973, V38, P317 CAPLUS
- (10) Eisenberg, M; Ann NY Acad Sci 1985, V447, P335 CAPLUS
- (11) Frigg, M; Poultry Science 1983, V63, P750
- (12) Gerbling; J Plant Physiol 1994, V143, P561 CAPLUS
- (13) Glassman; US 5258300 1993 CAPLUS
- (14) Gloeckler; US 5096823 1992 CAPLUS
- (15) Gloeckler, R; Gene 1990, V87, P63 CAPLUS
- (16) Knowles, J; Ann Rev BioChem 1989, V58, P195 CAPLUS
- (17) Kopinski, J; British Journal of Nutrition 1989, V62, P751 CAPLUS
- (18) Kopinski, J; Nutrition Reviews 1990, V48, P352
- (19) Levy-Schil, S; Appl Microbiol Biotechnol 1993, V38, P755 CAPLUS

- (20) Marshall, M; Nutrition Today Article 1987, V3, P26
- (21) Newman, T; Plant Physiol 1994, V106, P1241 CAPLUS
- (22) Otsuka, A; The Journal of Biological Chemistry 1988, V263, P19577 CAPLUS
- (23) Pai, C; J Bacteriol 1972, V112, P1280 CAPLUS
- (24) Patton; Mol Gen Genet 1966, V251, P261
- (25) Patton; Plant Physiol 1996, V112, P371 CAPLUS
- (26) Robel, E; Poultry Science 1991, V70, P1716 CAPLUS
- (27) Sakurai, N; J Biotech 1994, V36, P63 CAPLUS
- (28) Shellhammer, A; Oklahoma State University Thesis 1986, P1
- (29) Shiuan, D; Gene 1988, V67, P203 CAPLUS

L6 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2002 ACS

AN 1999:48059 CAPLUS

DN 130:107731

TI Method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes

IN Patton, David Andrew

PA Novartis Finance Corporation, USA

SO U.S., 28 pp., Cont.-in-part of U.S. Ser. No. 351,970, abandoned.
CODEN: USXXAM

DT Patent

LA English

IC ICM A01H005-00

ICS C12N005-04; C12N015-82

NCL 800205000

CC 11-2 (Plant Biochemistry)

Section cross-reference(s): 17

FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5859335	A	19990112	US 1995-401068	19950308
	WO 9617944	A2	19960613	WO 1995-EP4659	19951127
	WO 9617944	A3	19960829		
	W: AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, US, UZ, VN RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	CA 2205561	AA	19960613	CA 1995-2205561	19951127
	AU 9643001	A1	19960626	AU 1996-43001	19951127
	AU 700943	B2	19990114		
	EP 796337	A2	19970924	EP 1995-941628	19951127
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT,				
SE	JP 10510149	T2	19981006	JP 1995-517291	19951127
	US 5869719	A	19990209	US 1997-846338	19970430
	FI 9702336	A	19970606	FI 1997-2336	19970602
PRAI	US 1994-351970		19941208		
	US 1995-401068		19950308		
	WO 1995-EP4659		19951127		
AB	The present invention reveals that biotin biosynthesis in a plant is enhanced when the level of one or more of the enzymes in the plant biotin biosynthetic pathway is increased. Based upon this revelation methods which increase the level of one or more biotin biosynthetic enzymes in plant tissue are provided as a means for achieving enhanced levels of biotin in plant tissue. In particular, a method for enhancing biotin levels by introducing a chimeric gene, encoding chloroplast transit peptide fused to bacterial DAP				

aminotransferase or **biotin synthase**, into plant tissue is provided. Resulting transgenic plant tissue, including whole plants, having enhanced levels of biotin is also provided. Thus, Arabidopsis expressing Escherichia coli bioA gene produced twice as much biotin as control plants. The Arabidopsis bioB

was cloned and sequenced.

ST biotin prodn transgenic plant bioA bioB gene; sequence Arabidopsis gene bioB **biotin synthase** cDNA

IT Bacteria (Eubacteria)
Escherichia coli
(bioA or bioB genes of; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT Genes (microbial)
RL: BPR (Biological process); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)
(bioA; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT Genes (microbial)
RL: BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
(bioB; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT Chimeric genes
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(chloroplast transit peptide sequence-contg.; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT cDNA sequences
(for gene bioB **biotin synthase** of Arabidopsis)

IT Plant cells
(method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT Protein sequences
(of gene bioB **biotin synthase** of Arabidopsis)

IT Arabidopsis
Canola
Corn
Plant (Embryophyta)
Soybean (Glycine max)
Tobacco
Wheat
(transgenic; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT 179919-67-6
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT 37259-71-5P 80146-93-6P, **Biotin synthase**
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT 58-85-5, Biotin
RL: BOC (Biological occurrence); FFD (Food or feed use); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence); USES (Uses)

(method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

IT 179919-66-5
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (nucleotide sequence; method for enhancing biotin biosynthesis in plants and transgenic plants expressing chimeric bioA or bioB genes)

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
- (2) Anon; GB 2216530 1989 CAPLUS
- (3) Anon; EP 0635572 A2 1994 CAPLUS
- (4) Anon; WO 09408023 1994 CAPLUS
- (5) Baldet; Locus ATHSEACA 1995
- (6) Baldet, P; Eur J BioChem 1993, V217, P479 CAPLUS
- (7) Campbell; US 5445952 1995 CAPLUS
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- (11) Frigg, M; Poultry Science 1983, V63, P750
- (12) Gerbling; J Plant Physiol 1994, V143, P561 CAPLUS
- (13) Glassman; US 5258300 1993 CAPLUS
- (14) Gloeckler; US 5096823 1992 CAPLUS
- (15) Gloeckler, R; Gene 1990, V87, P63 CAPLUS
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- (18) Kopinski, J; Nutrition Reviews 1990, V48, P352
- (19) Levy-Schil, S; Appl Microbiol Biotechnol 1993, V38, P755 CAPLUS
- (20) Marshall, M; Nutrition Today Article 1987, V3, P26
- (21) Newman, T; Plant Physiol 1994, V106, P1241 CAPLUS
- (22) Otsuka, A; The Journal of Biological Chemistry 1988, V263, P19577 CAPLUS
- (23) Pai, C; J Bacteriol 1972, V112, P1280 CAPLUS
- (24) Robel, E; Poultry Science 1991, V70, P1716 CAPLUS
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- (27) Shiuan, D; Gene 1988, V67, P203 CAPLUS
- (28) Stryer, L; BioChemistry 1981, V2, P505
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- (30) Watanabe, K; Phytochemistry 1982, V21, P513 CAPLUS
- (31) Wolfner, M; J Mol Biol V96, P273 CAPLUS
- (32) Wu, A; Proc Natl Acad Sci U S 1978, V75, P5442 CAPLUS

L6 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS

AN 1996:494241 CAPLUS

DN 125:160360

TI Enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food

IN Patton, David Andrew

PA Ciba-Geigy A.-G., Switz.

SO PCT Int. Appl., 57 pp.
 CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N015-82
 ICS C12N015-52; C12N005-10; C12N005-04; A01H005-00

CC 3-2 (Biochemical Genetics)
 Section cross-reference(s): 7, 11, 17

FAN.CNT 3

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 9617944	A2	19960613	WO 1995-EP4659	19951127
	WO 9617944	A3	19960829		
	W: AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, US, UZ, VN				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	US 5859335	A	19990112	US 1995-401068	19950308
	AU 9643001	A1	19960626	AU 1996-43001	19951127
	AU 700943	B2	19990114		
	EP 796337	A2	19970924	EP 1995-941628	19951127
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT,				
SE	JP 10510149	T2	19981006	JP 1995-517291	19951127
	FI 9702336	A	19970606	FI 1997-2336	19970602
PRAI	US 1994-351970		19941208		
	US 1995-401068		19950308		
	WO 1995-EP4659		19951127		
AB	The present invention reveals that biotin biosynthesis in a plant is enhanced when the level of one or more of the enzymes in the plant biotin biosynthetic pathway is increased. Based upon this revelation methods which increase the level of one or more biotin biosynthetic enzymes in plant tissue are provided as a means for achieving enhanced levels of biotin in plant tissue. In particular, a method for enhancing biotin levels by introducing a chimeric gene capable of expressing a biotin biosynthetic enzyme into plant tissue is provided. Resulting transgenic plant tissue, including whole plants, having enhanced levels of biotin are also provided.				
ST	biotin formation genetic engineering plant enzyme				
IT	Gene, plant				
use,	RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)				
	(bioB; enhanced biotin formation in plant tissue, genetic engineering using increased enzyme formation, and transgenic plant as nutritional food)				
IT	Arabidopsis				
	Canola				
	Corn				
	Deoxyribonucleic acid sequences				
	Genetic engineering				
	Plant breeding and selection				
	Plant tissue				
	Protein sequences				
	Soybean				
	Tobacco				
	Wheat				
	(enhanced biotin formation in plant tissue, genetic engineering using increased enzyme formation, and transgenic plant as nutritional food)				
IT	Seed				
	(hybrid; enhanced biotin formation in plant tissue, genetic engineering using increased enzyme formation, and transgenic plant as nutritional food)				
IT	Chloroplast				

(targeting; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
 RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
 (bioA, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
 RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
 (bioB, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
 RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
 (bioC, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
 RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
 (bioD, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene, microbial
 RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
 (bioF, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Gene
 RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)
 (chimeric, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Genetic element
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (promoter, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Genetic element
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(terminator, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Transformation, genetic
(transgenic, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Peptides, biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(transit, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT Biological transport
(translocation, enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 120861-02-1P 179919-62-1P 179919-63-2P 179919-65-4P 179919-67-6P
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
PREP (Preparation); USES (Uses)
(amino acid sequence; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 120860-98-2
RL: PRP (Properties)
(amino acid sequence; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 9075-61-0P, 7-Keto-8-Aminopelargonic acid synthetase 37259-71-5P, 7,8-Diaminopelargonic acid aminotransferase 37259-75-9P, Desthiobiotin synthetase 55467-50-0P, Synthetase, pimelyl coenzyme A 80146-93-6P, **Biotin synthase**
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study);
PREP (Preparation); USES (Uses)
(enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 58-85-5P, Biotin
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); FFD (Food or feed use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 533-48-2, Desthiobiotin
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(enzyme converting desthiobiotin to 9-mercaptodesthiobiotin; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 179919-58-5 179919-61-0 179919-64-3 179919-66-5
RL: AGR (Agricultural use); BPR (Biological process); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process); USES (Uses)

(nucleotide sequence; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

IT 120859-43-0, Deoxyribonucleic acid (Escherichia coli gene bioD)
179919-59-6

RL: PRP (Properties)

(nucleotide sequence; enhanced biotin formation in **plant** tissue, genetic engineering using increased enzyme formation, and transgenic **plant** as nutritional food)

> d L9 bib

L9 ANSWER 1 OF 6 USPATFULL
AN 2002:38558 USPATFULL
TI Expressed sequences of arabidopsis thaliana
IN Gorlach, Jorn, Durham, NC, UNITED STATES
An, Yong-Qiang, San Diego, CA, UNITED STATES
Hamilton, Carol M., Apex, NC, UNITED STATES
Price, Jennifer L., Raleigh, NC, UNITED STATES
Raines, Tracy M., Durham, NC, UNITED STATES
Yu, Yang, Martinsville, NJ, UNITED STATES
Rameaka, Joshua G., Durham, NC, UNITED STATES
Page, Amy, Durham, NC, UNITED STATES
Mathew, Abraham V., Cary, NC, UNITED STATES
Ledford, Brooke L., Holly Springs, NC, UNITED STATES
Woessner, Jeffrey P., Hillsborough, NC, UNITED STATES
Haas, William David, Durham, NC, UNITED STATES
Garcia, Carlos A., Carrboro, NC, UNITED STATES
Kricker, Maja, Pittsboro, NC, UNITED STATES
Slater, Ted, Apex, NC, UNITED STATES
Davis, Keith R., Durham, NC, UNITED STATES
Allen, Keith, Cary, NC, UNITED STATES
Hoffman, Neil, Chapel Hill, NC, UNITED STATES
Hurban, Patrick, Raleigh, NC, UNITED STATES
PI US 2002023280 A1 20020221
AI US 2001-770444 A1 20010126 (9)
PRAI US 2000-178502P 20000127 (60)
DT Utility
FS APPLICATION
LREP PARADIGM GENETICS, INC, 104 ALEXANDER DRIVE, BUILDING 2, P O BOX 14528,
RTP, NC, 277094528
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 3845
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 19 2 bib

L9 ANSWER 2 OF 6 USPATFULL
AN 2001:199938 USPATFULL
TI **Plant biotin synthase**
IN Allen, Stephen M., Wilmington, DE, United States
Kinney, Anthony J., Wilmington, DE, United States
Miao, Guo-Hua, Johnston, IA, United States
Orozco, Emil M., JR., West Grove, PA, United States
PI US 2001039042 A1 20011108
AI US 2000-740288 A1 20001219 (9)
PRAI US 1999-172929P 19991221 (60)
DT Utility
FS APPLICATION
LREP E I DU PONT DE NEMOURS AND COMPANY, LEGAL DEPARTMENT - PATENTS, 1007
MARKET STREET, WILMINGTON, DE, 19898
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 2682
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 19 3 bib

L9 ANSWER 3 OF 6 USPATFULL
AN 2001:136414 USPATFULL
TI Method to produce biotin
IN Eddy, Christina K., Loveland, CO, United States
PA BASF Aktiengesellschaft, Ludwigshafen, Germany, Federal Republic of
(non-U.S. corporation)
PI US 6277609 B1 20010821
AI US 1993-1063 ✓ 19930106 (8)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Achutamurthy, Ponnathapu; Assistant Examiner: Moore,
William W.
LREP Whyte Hirschboeck Dudek SC
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 23 Drawing Page(s)
LN.CNT 2254
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 19 4 bib

L9 ANSWER 4 OF 6 USPATFULL
AN 1999:19377 USPATFULL
TI Transgenic plants having increased biotin content
IN Patton, David A., Durham, NC, United States
PA Novartis Finance Corporation, New York, NY, United States (U.S.
corporation) 105
PI US 5869719 19990209
AI US 1997-846338 19970430 (8)
RLI Continuation-in-part of Ser. No. US 1995-401068, filed on 8 Mar 1995,
now patented, Pat. No. US 5859335
DT Utility
FS Granted
EXNAM Primary Examiner: Robsinson, Douglas W.; Assistant Examiner: Zaghmout,
Ousama M-Faiz
LREP Meigs, J. Timothy
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 4 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1810
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 19 5 bib

L9 ANSWER 5 OF 6 USPATFULL
AN 1999:4985 USPATFULL
TI Enhanced biotin biosynthesis in plant tissue
IN Patton, David Andrew, Durham, NC, United States
PA Novartis Finance Corporation, New York, NY, United States (U.S.
corporation) 105
PI US 5859335 19990112
AI US 1995-401068 19950308 (8)
RLI Continuation-in-part of Ser. No. US 1994-351970, filed on 8 Dec 1994,
now abandoned
DT Utility

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 08:56:50 ; Search time 16.97 seconds

(without alignments)
814,534 Million cell updates/sec

Title: US-09-740-288A-22

Perfect score: 2206

Sequence: 1 MAMLLARNLRSLRPPLA.....EEVSAAPAESESEQAASM 377

Scoring table: PAM270

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1979	89.7	378	1	BIOB_ARATH
2	1369	62.1	363	1	BIOB_SCHPO
3	1253	56.8	346	1	BIOB_ECOLI
4	1247	56.5	346	1	BIOB_ERWHE
5	1237	56.1	346	1	BIOB_SERMA
6	1228	55.7	375	1	BIOB_YEAST
7	1184	53.7	343	1	BIOB_BUCAL
8	1154	52.3	333	1	BIOB_HAETIN
9	1102	50.0	341	1	BIOB_METSK
10	863	39.1	6359	1	BACC_BACLI
11	852	38.6	4568	1	DYHC_CHLRE
12	850	38.5	4644	1	DYHC_MOUSE
13	847	38.4	4644	1	DYHC_MOUSE
14	847	38.4	6486	1	TYCC_BACBR
15	843	38.2	4486	1	DYHC_HUMAN
16	840	38.1	4969	1	RYNC_RABIT
17	839	38.0	4367	1	DYHC_NEUCR
18	836	37.9	5065	1	EPPL_HUMAN
19	834	37.8	4540	1	DYHC_PASTE
20	834	37.8	5037	1	RYNC_RABIT
21	829	37.6	5035	1	RYNC_PIG
22	827	37.5	4725	1	DYHC_HUMAN
23	827	37.5	4725	1	DYHC_HUMAN
24	826	37.4	5032	1	DYHC_HUMAN
25	825	37.4	4439	1	PKSL_FUSO
26	823	37.3	4427	1	PKSL_FUSO
27	823	37.3	5255	1	BACC_BACLI
28	817	37.0	4485	1	DYHC_CHLRE
29	816	37.0	4128	1	PRKD_HUMAN
30	816	37.0	4465	1	DYHC_HUMAN
31	816	37.0	4639	1	DYHC_DROME
32	814	36.9	4036	1	RRPL_DUGBV
33	814	36.9	4568	1	DYHC_CAEEL

ALIGNMENTS

RESULT	ID	BIOS_ARATH	STANDARD	PRT	378 AA.
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DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DE	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).				
GN	BIO2 OR BIOB OR AT2G43360 OR T01024.10.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OX	NCBI_TaxID=3702;				
OX	NCBI_TaxID=3702;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. LANDSBERG ERECTA;				
RX	MEDLINE=96417082; PubMed=8619873;				
RA	Weaver L.M., Yu F., Mutele E.S., Nikolai B.J.;				
RT	"Characterization of the cDNA and gene coding for the biotin synthase				
RT	of Arabidopsis thaliana.";				
RL	Plant Physiol. 110:1021-1028(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLUMBIA; TISSUE=Leaf;				
RA	Patton D., Pacella M., Ward E.;				
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLUMBIA; TISSUE=Leaf;				
RA	MEDLINE=96307524; PubMed=8680961;				
RT	Baldet P., Ruffet M.L.;				
RT	"Biotin synthesis in higher plants: isolation of a cDNA encoding				
RT	Arabidopsis thaliana bioB gene product equivalent by functional				
RT	complementation of a biotin auxotroph mutant bioB105 of Escherichia				
RT	coli K12.";				
RL	C. R. Acad. Sci., III, Sci. Vie 319:99-106(1996).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLUMBIA;				
RX	MEDLINE=20083487; PubMed=10617197;				
RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,				
RA	Fuill C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,				
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,				
RA	Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Umayam L.,				
RA	Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,				
RA	Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,				
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,				
RT	Venter J.C.;				
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis				
RL	thaliana.";				
RL	Nature 402:761-768(1999).				
CC	-1- CATALYTIC ACTIVITY: DETHIOTIOTIN + (S) = BIOTIN.				
CC	-1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.				
CC	-1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES				
CC	FAMILY.				

34	814	36.9	4684	1	PLE1_HUMAN	Q15149 homo sapien
35	813	36.9	4447	1	PSK3_BACSU	P40803 bacillus su
36	810	36.7	362	1	BIOB_SYNZ3	P73538 synecocyst
37	808	36.6	3511	1	MY15_MOUSE	Q99224 mus musculu
38	808	36.6	4544	1	LRP1_HUMAN	Q07954 homo sapien
39	807	36.6	4829	1	BIR6_HUMAN	Q9nr09 homo sapien
40	807	36.6	5217	1	HTS1_COCCA	Q01886 coccolibolu
41	806	36.5	4466	1	DYHC_TRIGR	P23098 trypneustes
42	805	36.5	4393	1	PGBM_HUMAN	P98160 homo sapien
43	805	36.5	4753	1	LRP_CAEEL	Q04833 caenorhabdi
44	803	36.4	4273	1	PSKM_BACSU	P40872 bacillus su
45	803	36.4	4344	1	DYHC_EMENT	P45444 emericeella


```

CC -----
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CC -----
DR EMBL: U24147; AAA80226.1; -
DR EMBL: U31806; AAC49445.1; -
DR EMBL: L34413; AAB39953.1; -
DR EMBL: AC002335; AAB64312.1; -
DR InterPro: IPR002684; Biotin_synth.
DR Pfam: PF01792; Biotin_synth.1.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT METAL 94 94 IRON-SULFUR (POTENTIAL).
METAL 98 98 IRON-SULFUR (POTENTIAL).
METAL 101 101 IRON-SULFUR (POTENTIAL).
SQ SEQUENCE 378 AA; 41681 MW; B102E477E7353762 CRC64;

Query Match 89.7%; Score 1979; DB 1; Length 378;
Best Local Similarity 80.8%; Pred. No. 5,9e-38;
Matches 308; Conservative 49; Mismatches 10; Indels 14; Gaps 3;

QY 4 MLARN-LRSRLRPPLAA-----AAESSAAAEERAIROGPRNDMSRPETQAYDSP 55
DB 1 MMLVRSYFRSOLRPSVSGGLQASCYSSLSAAAEAEERTIREPRNDMSRDEIKSYDSP 60
QY 56 LLDLFFGAOVHNRVHKFREVOOCTLLSTIKTGCSSEDCSYCPSSRYNGLAKOKLMND 115
DB 61 LLDLFFGAOVHNRVHKFREVOOCTLLSTIKTGCSSEDCSYCPSSRYNGLAKOKLMND 120
QY 116 AVLEAAKAKESGSTRFCMGAAEMETIGKSNFNOILEYKEIRGMMEVCCTLGMIERO 175
DB 121 AVIDAAKKAKESGSTRFCMGAAEMETIGKSNFNOILEYKEIRGMMEVCCTLGMIERO 180
QY 176 QAEELKRGGLTAVNHNLDTSREYYPNITTRSDDDLOTLEHREAGISGSGITGLDE 235
DB 181 QAEELKRGGLTAVNHNLDTSREYYPNITTRSDDDLOTLEHREAGISGSGITGLDE 240
QY 236 AEDRVGLTLTLATLPTHPESVPINALVAVKGTPLLEDOKFVEIWEIMIRIATARTMPKA 295
DB 241 AEDRVGLTLTLATLPTHPESVPINALVAVKGTPLLEDOKFVEIWEIMIRIATARTMPKA 300
QY 296 MVRISAGVRFSMPDQALCFIAGANSIFPAGEKLLTTANNDPDDQAMFKLGLIPAPSE 355
DB 301 MVRISAGVRFSMPDQALCFIAGANSIFPAGEKLLTTANNDPDDQAMFKLGLIPAPSE 360
QY 356 GEEVSAAPAESERSEDOAS 376
DB 361 SEDD-----SESENCEKVAS 375

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ID BIOB_SCHPO STANDARD; PRT; 363 AA.
AC 059778; 060050;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN B102 OR SPCC120.01C OR SPCC1235.02.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=D18;
RX MEDLINE=99456674; PubMed=1052584;

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RA Philip V., Jeltsch J.M., Lemoine Y.;
RT "Cloning of Schizosaccharomyces pombe b102 by heterologous
RT complementation of a Saccharomyces cerevisiae mutant.";
RL Curr. Microbiol. 39:348-350(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA SRRIN-972;
RL Wood V., Rajandream M.A., Barrell B.G., Medier H., Wambutt R.;
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRIN-972;
RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: DEHYDROBIOTIN + (S) - BIOTIN.
CC -1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AJ224930; CA12229.1; -
DR EMBL: AL022245; CA11803.1; -
DR EMBL: AL031764; CA12106.1; -
DR InterPro: IPR002684; Biotin_synth.
DR Pfam: PF01792; Biotin_synth.1.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT METAL 69 69 IRON-SULFUR (POTENTIAL).
FT METAL 73 73 IRON-SULFUR (POTENTIAL).
FT METAL 76 76 IRON-SULFUR (POTENTIAL).
FT CONFLICT 13 14 SS -> FF (IN REF. 1).
FT CONFLICT 17 17 S -> F (IN REF. 1).
FT CONFLICT 312 318 TTPAVSW -> LLLFL (IN REF. 1).
SQ SEQUENCE 363 AA; 40650 MW; 00B2EDF901AEB1 CRC64;

Query Match 62.1%; Score 1369; DB 1; Length 363;
Best Local Similarity 52.8%; Pred. No. 5,3e-23;
Matches 204; Conservative 81; Mismatches 65; Indels 36; Gaps 6;

QY 5 LIARNLSRLRPPLAAAAAFSSAAAEERAIROG-----RNDMSRPEIQAYDSPILDL 60
DB 1 METTRIROLR-----RSSALSLVNNMTREIQRKIXDTPLDILDI 40
QY 61 FHGAOVHNRVHKFREVOOCTLLSTIKTGCSSEDCSYCPSSRYNGLAKOKLMNDVLEA 120
DB 41 FRAASIRHKFRDPKVVQOCTLLSTIKTGCTEDCKYCAQSSRYNGLAKOKLMNDVLEA 100
QY 121 AKKAKESGSTRFCMGAAEMETIGKSNFNOILEYKEIRGMMEVCCTLGMIERQAEEL 180
DB 101 AKKAKESGSTRFCMGSAWRDLNGRNRFFKNILLEIKFVRSMDEVCVTLGMEQAKEL 160
QY 181 KKAGITAVNHNLDTSREYYPNITTRSDDDLOTLEHREAGISGSGITGLGEAEEDR 240
DB 161 KDAGITAVNHNLDTSREYYPNITTRSDDDLOTLEHREAGISGSGITGLGEAEEDR 220
QY 241 VGLTLTLATLPTHPESVPINALVAVKGTPLLEDOKFVEIWEIMIRIATARTMPAMRV 298
DB 221 VGLTLTLATLPTHPESVPENLVIPGYPGDAVKERLPIHPFLRSIATARTICMPRTIIR 280
QY 299 LSAGVRFSMPDQALCFIAGANSIFPAGEKLLTTANNDPDDQAMFKLGLIPAPSE--- 355
DB 281 FAAGRNTSESEDOALAFAGANNAVTEKMLTTPAVSWDSOLFYNWGLEM-QSEFYG 339
QY 356 -----GEEVSAAPAESERSEDOAS 377
DB 340 TSTEGEDGTFILPP--KRLAPSPSL 363

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OM protein - protein search, using sw model

Run on: April 17, 2002, 08:59:13 ; Search time 16.97 Seconds

(without alignments)
814.534 Million cell updates/sec

Title: US-09-740-288A-24

Perfect score: 2212

Sequence: 1 MALMLIARNLRSLRPPLAA.....EASAAPTESEKSEQASM 377

Scoring table: PAM270

Gapop 10.0 , Gapext 0.0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1970	89.1	378	1	BIOB_ARATH
2	1360	61.5	363	1	BIOB_SCHPO
3	1242	56.1	346	1	BIOB_ECOLI
4	1233	55.7	346	1	BIOB_ERMHE
5	1230	55.6	346	1	BIOB_SERMA
6	1218	55.1	375	1	BIOB_YEAST
7	1175	53.1	343	1	BIOB_BUCAT
8	1143	51.7	333	1	BIOB_HAETN
9	1098	49.6	341	1	BIOB_METSK
10	862	39.0	6359	1	BACB_BACLI
11	857	38.7	4568	1	DYHC_CHIRE
12	854	38.6	4686	1	TYCC_BACBR
13	847	38.3	4969	1	RINC_RABIT
14	846	38.2	4644	1	DYHC_MOUSE
15	845	38.2	4647	1	DYHC_NEUCR
16	843	38.1	4644	1	DYHC_RAT
17	839	37.9	5037	1	RYNR_RABIT
18	839	37.9	5065	1	EPPL_HUMAN
19	838	37.9	4427	1	PKSL_BACSU
20	838	37.9	4486	1	DYHC_HUMAN
21	831	37.6	4725	1	DYHC_DICDI
22	831	37.6	5035	1	RYNR_PIG
23	831	37.6	5255	1	BACA_BACLI
24	830	37.5	5032	1	RYNR_HUMAN
25	828	37.4	4540	1	DYHC_PARTE
26	824	37.3	3530	1	MY15_HUMAN
27	823	37.2	4349	1	DYHC_FUSSO
28	821	37.1	4273	1	PKSM_BACSU
29	821	37.1	4485	1	DYHC_CHIRE
30	817	36.9	4684	1	RPEL_HUMAN
31	816	36.9	4036	1	RPEL_DUGAV
32	816	36.9	4447	1	PKSK_BACSU
33	815	36.8	4128	1	PRKD_HUMAN

ALIGNMENTS

RESULT	ID	BIOS_ARATH	STANDARD	PRT	378 AA
AC	P54967				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DT	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE)				
GN	BI02 OR BIOB OR ATG43360 OR T01024.10.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.				
OX	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. LANDSBERG ERECTA;				
RC	MEDLINE=96417082; PubMed=8819873;				
RA	Weaver L.M., Yu F., Wurtile E.S., Nikolau B.J.;				
RT	"Characterization of the cDNA and gene coding for the biotin synthase				
RT	of Arabidopsis thaliana.";				
RL	Plant Physiol. 110:1021-1028(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLUMBIA; TISSUE=leaf;				
RC	Pattison D., Paccella M., Ward E.;				
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLUMBIA; TISSUE=leaf;				
RC	MEDLINE=96307524; PubMed=8680961;				
RA	Balder P., Ruffet M.L.;				
RT	"Biotin synthesis in higher plants: isolation of a cDNA encoding				
RT	Arabidopsis thaliana bioh-gene product equivalent by functional				
RT	complementation of a biotin auxotroph mutant bioh105 of Escherichia				
RT	coli K12.";				
RL	C. R. Acad. Sci., III, Sci. Vie 319:99-106(1996).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLUMBIA;				
RC	MEDLINE=20083487; PubMed=10617197;				
RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Bentle M.-I., Town C.D.,				
RA	Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,				
RA	Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,				
RA	Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Umayah R.L.,				
RA	Tallon J.E., Gili J.E., Adams M.D., Carrera A.J., Greasy T.H.,				
RA	Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,				
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,				
RA	Venter J.C.;				
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis				
RT	thaliana.";				
RL	Nature 402:761-768(1999).				
CC	-1- CATALYTIC ACTIVITY: DEHYDROBIOTIN + (S) = BIOTIN.				
CC	-1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.				
CC	-1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES				
CC	FAMILY.				

Q19020 caenorhabd
P39057 anthocidari
P98157 gallus gall
P73538 synecocyst
P37276 drosophila
Q01886 cochllobolu
Q07954 homo sapien
P30427 rattus norv
P45444 emeritella
P23098 tripneustes
Q04833 caenorhabd
Q9qrx20 mus musculu

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 CC or send an email to license@isb-sib.ch).

DR EMBL: U24147; AAA80226.1; -
 DR EMBL: U31806; AAC49445.1; -
 DR EMBL: L34413; AAB39953.1; -
 DR EMBL: AC002335; AAB64312.1; -
 DR InterPro: IPR002684; Biotin_synth.
 DR Pfam: PF01792; Biotin_synth.1.
 KW Biotin biosynthesis; Iron-sulfur; Transferrase.
 FT METAL 94
 FT METAL 98
 FT METAL 101
 FT METAL 101
 SEQUENCE 378 AA; 41681 MW; B102E477E7353762 CRC64;

Query Match 89.1%; Score 1970; DB 1; Length 378;
 Best Local Similarity 80.6%; Pred. No. 7e-37;
 Matches 307; Conservative 49; Mismatches 11; Indels 14; Gaps 3;

QY 4 MLARN-LRSRLRPPLAA-----AFSSAAAEARAIIDGPRDMSRPEIQAYTDP 55
 DB 1 MLVRSVRSQLRPSVSGLOSASCYSLSAASAEETITIEGRNDSRDEIKSYDSP 60
 QY 56 LLDLIFGAQVHRVNHKREYQOCTLSIKTGSCSEDCSYCPOSSRYNTGKAKNKX 115
 DB 61 LLDLIFGAQVHRVNHKREYQOCTLSIKTGSCSEDCSYCPOSSRYNTGKAKNKX 120
 QY 116 AVEAAKAKKESGSTRFCMGAMRETIIGKSNFQIIEYKEIRGMGEVCTGMIETK 175
 DB 121 AVIDAAKAKKESGSTRFCMGAMRETIIGKSNFQIIEYKEIRGMGEVCTGMIETK 180
 QY 176 QAELKRAKGLTAYNNHNDTSEYEPNITITTSYDRLQTEHREAGISICSGGII 235
 DB 181 QAELKRAKGLTAYNNHNDTSEYEPNITITTSYDRLQTEHREAGISICSGGII 240
 QY 236 AEDRVGLTATLPTPEVSPINAVVAGTPLEDOKPEIEMTBMATATITMPKA 295
 DB 241 AEDRVGLTATLPTPEVSPINAVVAGTPLEDOKPEIEMTBMATATITMPKA 300
 QY 296 MVRLSAGRVRSMEQALCFIAGANSIFAGKELTTANNDPADQAMFKILGIPKAPF 355
 DB 301 MVRLSAGRVRSMEQALCFIAGANSIFAGKELTTANNDPADQAMFKILGIPKAPF 360
 QY 356 GEEFASAAAPTESERSEQAAS 376
 DB 361 SEDD-----SESENCEKVAS 375

RESULT 2
 BIOR_SCHPO STANDARD; PRT; 363 AA.
 AC 059778; 060050;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
 GN B102 OR SPC320.01C OR SPC1235.02.
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN (1)
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RC STRAIN-D18;
 RX MEDLINE=99456674; PubMed=1052584;

RA Philip V., Jeltsch J.M., Lemoine Y.;
 RT "Cloning of Schizosaccharomyces pombe b102 by heterologous
 RL complementation of a Saccharomyces cerevisiae mutant.";
 RN Curr. Microbiol. 39:348-350(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Wood V., Rajandream M.A., Barrell B.G., Wedler H., Wambutt R.;
 RL Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
 RL Submitted (Sep-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: DETHYBIOTIN + (S) - BIOTIN.
 CC -1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
 CC FAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: AJ224930; CA112229.1; -
 DR EMBL: AL022245; CA118303.1; -
 DR EMBL: AL031764; CA121106.1; -
 DR InterPro: IPR002684; Biotin_synth.
 DR Pfam: PF01792; Biotin_synth.1.
 KW Biotin biosynthesis; Iron-sulfur; Transferrase.
 FT METAL 69
 FT METAL 73
 FT METAL 76
 FT METAL 76
 FT CONFLICT 13
 FT CONFLICT 14
 FT CONFLICT 17
 FT CONFLICT 312
 FT CONFLICT 318
 SEQUENCE 363 AA; 40650 MW; 008E2EDF9901AEB1 CRC64;

Query Match 61.5%; Score 1360; DB 1; Length 363;
 Best Local Similarity 52.6%; Pred. No. 3.3e-22;
 Matches 203; Conservative 82; Mismatches 65; Indels 36; Gaps 6;

QY 5 LIAARNRSRLRPPLAAAFSSAAAEARAIIDGPRDMSRPEIQAYTDP 60
 DB 1 MFTKTRQOIR-----RSSALSLVRNMTREETQKTYDTPLDL 40
 QY 61 FHGAQVHRVNHKREYQOCTLSIKTGSCSEDCSYCPOSSRYNTGKAKNKXAVLEA 120
 DB 41 FRAASIHRRFHDPKKQYQOCTLSIKTGSCSEDCSYCPOSSRYNTGKAKNKXAVLEA 100
 QY 121 AKKAKESGSTRFCMGAMRETIIGKSNFQIIEYKEIRGMGEVCTGMIETK 180
 DB 101 AKKAKESGSTRFCMGAMRETIIGKSNFQIIEYKEIRGMGEVCTGMIETK 160
 QY 181 KRAKGLTAYNNHNDTSEYEPNITITTSYDRLQTEHREAGISICSGGII 240
 DB 161 KRAKGLTAYNNHNDTSEYEPNITITTSYDRLQTEHREAGISICSGGII 220
 QY 241 VGLIHLATLPTPEVSPINAVVAGTPLED--OKPVEIWMIMYATARTMPKAMVR 298
 DB 221 VGLIHLATLPTPEVSPINAVVAGTPLED--OKPVEIWMIMYATARTMPKAMVR 280
 QY 299 LSAGRVRSMEQALCFIAGANSIFAGKELTTANNDPADQAMFKILGIPKAPF--- 355
 DB 281 LSAGRVRSMEQALCFIAGANSIFAGKELTTANNDPADQAMFKILGIPKAPF--- 339
 QY 356 -----GEEFASAAAPTESERSEQAAS 377
 DB 340 TSTEGEDGTFTLP--KERLAPSPSL 363

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OM protein - protein search, using sw model

Run on: April 17, 2002, 08:59:13 ; Search time 16.97 Seconds

(without alignments)
814,534 Million cell updates/sec

Title: US-09-740-288a-24

Perfect score: 2212
Sequence: 1 MALMLARNLRSLRPLA.....EASAAAPTESERSEQASM 377

Scoring table: PAM270
Gapop 10.0, Gapext 0.0

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1970	89.1	378	1	BIOB_ARATH
2	1360	61.5	363	1	BIOB_SCHPO
3	1242	56.1	346	1	BIOB_ECOLI
4	1233	55.7	346	1	BIOB_ERMHE
5	1230	55.6	346	1	BIOB_SERMA
6	1218	55.1	375	1	BIOB_YEAST
7	1175	53.1	343	1	BIOB_BUCAL
8	1143	51.7	333	1	BIOB_HAELN
9	1098	49.6	341	1	BIOB_METSK
10	862	39.0	6359	1	BACG_BACLI
11	857	38.7	4568	1	DYHC_CHLRE
12	854	38.6	6486	1	TYCC_BACBR
13	847	38.3	4969	1	RINC_RABIT
14	846	38.2	4644	1	DYHC_MOUSE
15	845	38.2	4367	1	DYHC_NEUCR
16	843	38.1	4644	1	DYHC_RAT
17	839	37.9	5037	1	RYNR_RABIT
18	839	37.9	5065	1	EPLL_HUMAN
19	838	37.9	4427	1	PKSL_BACSU
20	838	37.9	4486	1	DYHC_HUMAN
21	831	37.6	4725	1	DYHC_DICDI
22	831	37.6	5035	1	RYNR_PIG
23	831	37.6	5255	1	BACA_BACLI
24	830	37.5	5032	1	RYNR_HUMAN
25	828	37.4	4540	1	DYHC_PARTE
26	824	37.3	3530	1	MY15_HUMAN
27	823	37.2	4349	1	DYHC_FUSSO
28	821	37.1	4273	1	PKSM_BACSU
29	821	37.1	4485	1	DYHC_CHLRE
30	817	36.9	4684	1	PELI_HUMAN
31	816	36.9	4036	1	RPLD_DUGAV
32	816	36.9	4447	1	PKSK_BACSU
33	815	36.8	4128	1	PRKD_HUMAN

34	814	36.8	4568	1	DYHC_CAEEL	Q19020 caenorhabdi
35	813	36.8	4466	1	DYHC_ANTCR	P39057 antioctidari
36	813	36.8	4543	1	LRPI_CHICK	P98157 gallus gall
37	811	36.7	362	1	BIOB_SYNY3	P73538 synechocyst
38	811	36.7	4639	1	DYHC_DROME	P37276 drosophila
39	811	36.7	5217	1	HTSI_COCCA	Q01886 cochlilobolu
40	809	36.6	4544	1	LRPI_HUMAN	Q07954 homo sapien
41	809	36.6	4687	1	PLEI_RAT	P30427 rattus norv
42	808	36.5	4344	1	DYHC_EMENT	P45444 emeritella
43	807	36.5	4466	1	DYHC_PRICR	P23098 tripteneusta
44	807	36.5	4753	1	LRP_CAEEL	Q04833 caenorhabdi
45	807	36.5	5327	1	ACE7_MOUSE	Q9qrx0 mus musculu

ALIGNMENTS

RESULT	ID	BIOS	ARATH	STANDARD	PRT	378 AA.
AC	P54967					
DT	01-OCT-1996	(Rel. 34, Created)				
DT	01-OCT-1996	(Rel. 34, Last sequence update)				
DT	20-AUG-2001	(Rel. 40, Last annotation update)				
DE	BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).					
GN	BIOT OR BIOB OR ATG43360 OR T01024.10.					
OS	Arabidopsis thaliana (Mouse-ear cress).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;					
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.					
OX	NCBI_Taxid=3702;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-CV. LANDSBERG. ERECTA.					
RX	MEDLINE=96417062; Pubmed=8819873;					
RA	Weaver L.M., Yu F., Wurtile E.S., Nikolau B.J.;					
RT	"Characterization of the cDNA and gene coding for the biotin synthase					
RT	of Arabidopsis thaliana.";					
RL	Plant Physiol. 110:1021-1026(1996).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-CV. COLUMBIA; TISSUE=leaf;					
RA	Patton D., Pacella M., Ward E.;					
RT	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-CV. COLUMBIA; TISSUE=leaf;					
RX	MEDLINE=96307524; Pubmed=8680961;					
RA	Balder P., Ruffet M.L.;					
RT	"Biotin synthesis in higher plants: Isolation of a cDNA encoding					
RT	Arabidopsis thaliana biob-gene product equivalent by functional					
RT	complementation of a biotin auxotroph mutant bioB105 of Escherichia					
RL	coli K12.";					
RN	C. R. Acad. Sci., III, sci. Vie 319:99-106(1996).					
RP	[4]					
RC	SEQUENCE FROM N.A.					
RX	STRAIN-CV. COLUMBIA;					
RA	MEDLINE=20083487; Pubmed=10617197;					
RA	Liu X., Kaul S., Rounsley S.D., Shea T.P., Beato M.-I., Town C.D.,					
RA	Fuji C.Y., Mason T.K., Bowman C.L., Barnstead M.E., Feldlyum T.V.,					
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,					
RA	Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Unayam L.,					
RA	Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,					
RA	Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,					
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,					
RT	Venter J.C.;					
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis					
RT	thaliana.";					
RL	Nature 402:761-768(1999).					
CC	-1- CATALYTIC ACTIVITY: DEHYDROBIOTIN + (S) = BIOTIN.					
CC	-1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.					
CC	-1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES					
CC	FAMILY.					

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 CC -----
 DR EMBL; U24147; AAA80226.1; -
 DR EMBL; U31806; AAC49445.1; -
 DR EMBL; L34413; AAB39953.1; -
 DR EMBL; AC002335; AAB64312.1; -
 DR InterPro: IPR002684; Biotin_synth.
 DR Pfam; PF01792; Biotin_synth; 1.
 DR Biotin biosynthesis; Iron-sulfur; transferase.
 FT METAL 94
 FT METAL 98
 FT METAL 101
 FT METAL 101
 SEQUENCE 378 AA; 41681 MW; B102B477E735762 CRC64;

Query Match 89.1%; Score 1970; DB 1; Length 378;
 Best Local Similarity 80.6%; Pred. No. 7e-37;
 Matches 307; Conservative 49; Mismatches 11; Indels 14; Gaps 3;

OY 4 MLARN-LRSLRPLPLAA-----AAFSAAAEERAIKDFGRNDSPREIOAVYDSP 55
 DB 1 MLVNSVRSOLRPSVSGLOSASCYSLSNAASAERETIEGRNDSPREIKSVYDSP 60
 OY 56 LLDLFFHGAOVHRNHYKREYVOOCTLLSIKGGSEDCSYCPOSSRYNTGLKAKLNNKY 115
 DB 61 LLDLFFHGAOVHRNHYKREYVOOCTLLSIKGGSEDCSYCPOSSRYNTGLKAKLNNKY 120
 OY 116 AVLEAKAKAKESGSTRFCMGAMRETIKRSNFOILEYVEIKMGMEVCCITGMIEKY 175
 DB 121 AVIDAKAKAKESGSTRFCMGAMRETIKRSNFOILEYVEIKMGMEVCCITGMIEKY 180
 OY 176 QAELEKKGGLAANNHNTLSREYPINTTTSYDRLOTLEHVEADAGISTGSGITGLGE 235
 DB 181 QAELEKKGGLAANNHNTLSREYPINTTTSYDRLOTLEHVEADAGISTGSGITGLGE 240
 OY 236 AAEEDVGLHTLATLPTPESVPINAVAVKGTPLDOKPVEIEMIRMIATARTMPKA 295
 DB 241 AAEEDVGLHTLATLPTPESVPINAVAVKGTPLDOKPVEIEMIRMIATARTMPKA 300
 OY 296 MVRISAGVRFSMPBALCFLAGANSIFAGEKLLTTANNDDADQAMFKILGLIPKAPSF 355
 DB 301 MVRISAGVRFSMPBALCFLAGANSIFAGEKLLTTANNDDADQAMFKILGLIPKAPSF 360
 OY 356 GEEEAASAPTESERSEQAAS 376
 DB 361 SEED-----SESENCERVAAS 375

RESULT 2
 BIOB_SCHPO STANDARD: PRT: 363 AA.
 AC 059778; 060050;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
 GN B102 OR SPEC320.01C OR SPEC1235.02.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomyces.
 OX NCBI_Taxid=4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN-D18;
 RX MEDLINE=99456674; PubMed=1052584;

RA Philip V., Jeltsch J.M., Lemoine Y.;
 RT "Cloning of Schizosaccharomyces pombe b102 by heterologous
 RT complementation of a Saccharomyces cerevisiae mutant.";
 RL Curr. Microbiol. 39:348-350(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA Wood V., Rajandream M.A., Barrell B.G., Wedler H., Wambutt R.;
 RA Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
 RA Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) - BIOTIN.
 CC -1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
 CC FAMILY.
 CC -----
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 CC -----

DR EMBL; AJ224930; CAA12229.1; -
 DR EMBL; AL022245; CAA18303.1; -
 DR EMBL; AL031764; CAA21106.1; -
 DR InterPro: IPR002684; Biotin_synth.
 DR Pfam; PF01792; Biotin_synth; 1.
 DR Biotin biosynthesis; Iron-sulfur; transferase.
 FT METAL 69
 FT METAL 73
 FT METAL 76
 FT METAL 13
 FT CONFLICT 17
 FT CONFLICT 17
 FT CONFLICT 312
 SEQUENCE 363 AA; 40650 MW; 008E2BDF901AEB1 CRC64;

Query Match 61.5%; Score 1360; DB 1; Length 363;
 Best Local Similarity 52.6%; Pred. No. 3.3e-22;
 Matches 203; Conservative 82; Mismatches 65; Indels 36; Gaps 6;

OY 5 LLARNLRSLRPLPLAA-----AAFSAAAEERAIKDFGRNDSPREIOAVYDSP 60
 DB 1 MFRTRIRQGR-----SSALSLVRNNMTREELKIDYDFLIDLI 40
 OY 61 FHGAOVHRNHYKREYVOOCTLLSIKGGSEDCSYCPOSSRYNTGLKAKLNNKYAVTEA 120
 DB 41 FRAASHRKHPDKKVOOCTLLSIKGGCTEDCKCAOSSRYNTGVKATKIKKIDIEVELEK 100
 OY 121 AKKAKESGSTRFCMGAMRETIKRSNFOILEYVEIKMGMEVCCITGMIEKQAEEL 180
 DB 101 AKTAKAKGSTRFCMGAMRETIKRSNFOILEYVEIKMGMEVCCITGMIEKQAEEL 160
 OY 181 KKAAGLTAYNNHNTLSREYPINTTTSYDRLOTLEHVEADAGISTGSGITGLGAEAEER 240
 DB 161 KKAAGLTAYNNHNTLSREYPINTTTSYDRLOTLEHVEADAGISTGSGITGLGAEAEER 220
 OY 241 VGLHTLATLPTPESVPINAVAVKGTPLDOKPVEIEMIRMIATARTMPKAMVR 298
 DB 221 VGLHTLATLPTPESVPINAVAVKGTPLDOKPVEIEMIRMIATARTMPKAMVR 280
 OY 299 LSGARVRFSMPBALCFLAGANSIFAGEKLLTTANNDDADQAMFKILGLIPKAPSF 355
 DB 281 LSGARVRFSMPBALCFLAGANSIFAGEKLLTTANNDDADQAMFKILGLIPKAPSF 339
 OY 356 -----GEEEAASAPTESERSEQAAS 377
 DB 340 TSTEGEDGRTTLP--KERLAPSPSL 363

1000

description
P54967 arbidolactis
O59797 schizosaccharis
P12996 escherichia
Q47862 evyria mar
P36569 serratia mar
P32451 saccharomon
P57378 buchnera ap
P44987 haemophilus
P49466 methylobact
O68008 b bacillact
O39565 chlamydomon
Q39144 mus musculu
P38650 rattus norveg
O30409 b tyrocidin
Q39057 homo sapien
P30957 cryptocogla
P54543 neurospora
P58107 homo sapien
Q27171 paramoelium
P11716 cryptocogla
P16960 sus scrofa
Q34036 homo sapien
P21817 dictyostell
P78716 insarillum su
O05470 bacillus su
O68006 b bacillact
Q39575 chlamydomon
P78527 homo sapien
P39057 antiocheta
P37276 dtrosophila
O66431 duges habibi
O19020 caenorhabdi

CC -1- SIMILARITY: BELONGS TO THE BI

ALIGNMENTS			
1	2	3	4
ARATH	STANDARD	PRT	378 AA.
P54967	01-OCT-1996 (Rel. 34, Created)		
	01-OCT-1996 (Rel. 34, last annotation update)		
	20-AUG-2001 (Rel. 40, last annotation update)		
	BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).		
	B102 OR B10B OR AT2G43360 OR T01024.10.		
	Arabidopsis thaliana (Mouse-ear cress).		
	Arabidopsis thaliana (Mouse-ear cress).		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.		
	NCBI_TaxID=3702.		
[1]	SEQUENCE FROM N.A.		
	STRAIN-CV. LANDSBERG ERRECTA.		
	MEDLINE=96417082; PubMed=8819873;		
	Weaver L.M., Yu F., Wurtele E.S., Nikolau B.J.;		
	"Characterization of the cDNA and gene coding for the biotin synthase of Arabidopsis thaliana."		
	Plant Physiol. 110:1021-1028(1996).		
[2]	SEQUENCE FROM N.A.		
	STRAIN-CV. COLUMBIA; TISSUE=leaf;		
	Patton D., Pacella M., Ward E.;		
	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.		
[3]	SEQUENCE FROM N.A.		
	STRAIN-CV. COLUMBIA; TISSUE=leaf;		
	MEDLINE=96307524; PubMed=8660961;		
	Balder P., Ruffet M.L.;		
	"Biotin synthetase in higher plants: isolation of a cDNA encoding Arabidopsis thaliana bioB-gene product equivalent by functional complementation of a biotin auxotroph mutant b10b105 of Escherichia coli K12."		
	C.R. Acad. Sci., III. Ser. Vie 319:99-106(1996).		
[4]	SEQUENCE FROM N.A.		
	STRAIN-CV. COLUMBIA;		
	MEDLINE=20083487; PubMed=10617197;		
	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eilen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;		
	"Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."		
	Nature 402:761-768(1999).		
-1-	CATALYTIC ACTIVITY: DEHYDROBIOTIN + (S) - BIOTIN.		
-1-	PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.		
-1-	SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES FAMILY.		

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CC -----
DR EMBL: U24147; AAA80226.1; -
DR EMBL: U31806; AAC49445.1; -
DR EMBL: L34413; AAB39953.1; -
DR EMBL: AC002335; AAB64312.1; -
DR InterPro: IPR002684; Biotin_synth.
DR Pfam: PF01792; Biotin_synth; 1.
KW Biotin biosynthesis; Iron-sulfur; Transferrase.
FT METAL 94 94 IRON-SULFUR (POTENTIAL).
FT METAL 98 98 IRON-SULFUR (POTENTIAL).
FT METAL 101 101 IRON-SULFUR (POTENTIAL).
SQ SEQUENCE 378 AA; 41681 MW; B102E477E7353762 CRC64;

Query Match 89.7%; Score 1979; DB 1; Length 378;
Best Local Similarity 80.8%; Pred. No. 5,9e-38;
Matches 308; Conservative 49; Mismatches 10; Indels 14; Gaps 3;

QY 4 MLTARN-LRSRLRPPLAA-----AFSSAAAEERAIKDRGRNDMSRPEIQAYVDS 55
DB 1 MMLVRSYFRQQLARPSVSGGQSASCSLSAASAEERITREGPRNDMSDEIKSYVDS 60
QY 56 LLDLLEFGAIVHNRHNFREVOQCTLLSIKIGGSEDCSYCPQSSRYNTGLAKQKLNMD 115
DB 61 LLDLLEFGAIVHNRHNFREVOQCTLLSIKIGGSEDCSYCPQSSRYNTGLAKQKLNMD 120
QY 116 AVEAAKAKESSTRPCMGAAERITGRKSNQILEYKELRGGMVECTGLMIEQ 175
DB 121 AVDAKAAKAEASTRCMGAAERITGRKSNQILEYKELRGGMVECTGLMIEQ 180
QY 176 QAEELKAGLTAVNHNLDTSREYYPNITRSDRLQTEHREAGISGSGIIGLGE 235
DB 181 QAEELKAGLTAVNHNLDTSREYYPNITRSDRLQTEHREAGISGSGIIGLGE 240
QY 236 AEDRGLTLTLTPHESPVPINALVAVKGPLEDQKPEVEMIMATARTIMPKA 295
DB 241 AEDRGLTLTLTPHESPVPINALVAVKGPLEDQKPEVEMIMATARTIMPKA 300
QY 296 MVLRSAGRVFSPEDQALCTLAGANSIFAGEKLLTANDEFDAQMFKILGIPKAPSF 355
DB 301 MVLRSAGRVFSPEDQALCTLAGANSIFAGEKLLTANDEFDAQMFKILGIPKAPSF 360
QY 356 GEEVSAAPAESESRSEAOAS 376
DB 361 SEDD-----SESENCEKVAS 375

RESULT 2
BIOB_SCHPO STANDARD: PRT: 363 AA.
AC 059778; 060050;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
GN B102 OR SPC320.01C OR SPC1235.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
ON NCBI_TaxID=4896;
RX [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN-D18;
MEDLINE=99456674; PubMed=1052584;

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RA Philip V., Jeltsch J.M., Lemoine Y.;
RT "Cloning of Schizosaccharomyces pombe bio2 by heterologous
RT complementation of a Saccharomyces cerevisiae mutant.";
RL Curr. Microbiol. 39:348-350(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Wood V., Rajandream M.A., Barrell B.G., Wiedler H., Wambutt R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) - BIOTIN.
CC -1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPIC ACID SYNTHETASES
CC FAMILY.
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CC -----
DR EMBL: AJ224930; CAA12229.1; -
DR EMBL: AL022245; CAA18303.1; -
DR EMBL: AL031764; CAA21106.1; -
DR InterPro: IPR002684; Biotin_synth.
DR Pfam: PF01792; Biotin_synth; 1.
KW Biotin biosynthesis; Iron-sulfur; Transferrase.
FT METAL 69 69 IRON-SULFUR (POTENTIAL).
FT METAL 73 73 IRON-SULFUR (POTENTIAL).
FT METAL 76 76 IRON-SULFUR (POTENTIAL).
FT CONFLICT 13 14 SS -> FE (IN REF. 1).
FT CONFLICT 17 17 S -> F (IN REF. 1).
FT CONFLICT 312 318 TTPAVSW -> LLDLFL (IN REF. 1).
SQ SEQUENCE 363 AA; 40650 MW; 008E2EDF9901AEB1 CRC64;

Query Match 62.1%; Score 1369; DB 1; Length 363;
Best Local Similarity 52.8%; Pred. No. 5.3e-23;
Matches 204; Conservative 81; Mismatches 65; Indels 36; Gaps 6;

QY 5 LLARNLRSRLRPPLAAAAAFSSAAAEERAIKDRP-----RNDMSRPEIQAYVDSPLDLL 60
DB 1 METRIRIQIR-----RSSALSLVRNNMREIQRIYDPLDLI 40
QY 61 FHGAOVHNRHNFREVOQCTLLSIKIGGSEDCSYCPQSSRYNTGLAKQKLNDAVLEA 120
DB 41 FRASIHRRKFDHPKRVQCTLLSIKIGGSEDCSYCAQSSRYNTGLAKQKLNDAVLEA 100
QY 121 AKKAKESSTRPCMGAAERITGRKSNQILEYKELRGGMVECTGLMIEQ 180
DB 101 AKIARAKSSTRPCMGSAARDLNGRNRTFKNLEIKERSHDEVCYTLNLDQAKEL 160
QY 181 KAGLTAVNHNLDTSREYYPNITRSDRLQTEHREAGISGSGIIGLGEAEEDR 240
DB 161 KDAGLTAVNHNLDTSREYYSKIISTRTYDERLNTIDNLRKAGLKVCGGILGEEKHDR 220
QY 241 VGLLHTLATLTPHESPVPINALVAVKGPLED--QKPEVEMIMATARTIMPKAMVR 298
DB 221 VGLHSLATMPTPHESPVPNLVPIPGPDADAKERLPIHPFLRSIATARIQMPKTIIR 280
QY 299 LSAGRVFSPEDQALCTLAGANSIFAGEKLLTANDEFDAQMFKILGIPKAPSF--- 355
DB 281 FAAGRNTCSSESOALAFAGANNAVFTGEKMLTTPAVSWDSOULEYMWGLEM-QSEFYG 339
QY 356 ---GEEVSAAPAESESRSEAOASM 377
DB 340 TSTGEDEGTFLRP--KERLAPSPSL 363

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